

Amendments to the Specification:

Please replace the sequence listing with the amended sequence listing submitted herewith.

Please replace the third paragraph on page 13 of the application as filed with the following amended paragraph:

Figure 2 shows the alignment of the DNA sequences depicted in SEQ ID NO:1 (BNM3A) and SEQ ID NO:3 (BNM3B). The ATG and TAG translation initiation and translation termination codons are shown in bold. Identical nucleotides are indicated by (*) and gaps are indicated by (-).

Please replace the fourth paragraph on page 13 of the application as filed with the following amended paragraph:

Figure 3 shows the alignment of the predicted protein sequences (SEQ ID NO:2 (BNM3A); SEQ ID NO:4 (BNM3B)) encoded by the DNA of SEQ ID NO:1 (BNM3A) and SEQ ID NO:3 (BNM3B). The amino acid sequence of the first AP2 domain repeat (repeat 1) and the second AP2 domain repeat (repeat 2), are shown in bold. Identical amino acids are indicated by an asterisk (*) and mismatches by a dot (.) below the sequence alignment.

Please replace the first paragraph on page 14 of the application as filed with the following amended paragraph:

Figure 5 shows the alignment of the predicted protein sequence encoded by the DNA of SEQ ID NO[.]:1 (BNM3A) with the predicted protein sequences of other AP2 domain proteins. The amino acid sequence of BNM3A, beginning at position 208, and spanning the first AP2 domain repeat (AP2 domain repeat 1; amino acids 208-284 of SEQ ID NO:2), the second AP2 domain repeat (AP2 domain repeat 2; amino acids 310-378 of SEQ ID NO:2), and the linker region lying between the two repeats (linker; amino acids 285-309 of SEQ ID NO:2), was aligned with the amino acid sequence of other proteins containing two AP2 domains; ANT (AP2 domain repeat 1 (amino acids 281-357 of SEQ ID

NO:15); linker (amino acids 358-382 of SEQ ID NO:15); AP2 domain repeat 2 (amino acids 383-451 of SEQ ID NO:15); ZM (AP2 domain repeat 1 (amino acids 138-214 of SEQ ID NO:16); linker (amino acids 215-239 of SEQ ID NO:16); AP2 domain repeat 2 (amino acids 240-308 of SEQ ID NO:16)); GL15 (AP2 domain repeat 1 (amino acids 111-177 of SEQ ID NO:17); linker (amino acids 178-202 of SEQ ID NO:17); AP2 domain repeat 2 (amino acids 203-270 of SEQ ID NO:17)); AP2 (AP2 domain repeat 1 (amino acids 129-195 of SEQ ID NO:18); linker (amino acids 196-220 of SEQ ID NO:18); AP2 domain repeat 2 (amino acids 221-288 of SEQ ID NO:18). The amino acid similarity in this region ranges from 53% for APETALA2 to 80% for ZMMHCF1. Identical amino acids are indicated by (*) and gaps are indicated by (-). Protein names are indicated on the left and are abbreviated as follows: ANT, A^{IN}TEGUMENTA (accession number U41339); ZM, ZMMHCF1 (accession number Z47554); GL15, GLOSSY15 (accession number U41466); AP2, APETALA2 (accession number U12546).

Please replace the fourth paragraph on page 23 of the application as filed with the following amended paragraph:

Such homology determinations may be made using oligonucleotide alignment algorithms for example, but not limited to a BLAST (~~GenBank URL: www.ncbi.nlm.nih.gov/egi-bin/BLAST/~~, using default parameters: Program: blastn; Database: nr; Expect10; filter: default; Alignment: pairwise; Query genetic Codes: Standard (1)) or FASTA, again using default parameters. Using sequence similarity searches *AtBBM* exhibits about 85% homology with the full length of *BNM3*, and therefore, *AtBBM* is a *BNM3* gene. Furthermore, a *BNM3* gene may also be defined in terms of its ability to hybridize with sequences disclosed in the present invention. Therefore, “*BNM3*” or “*BNM3* gene”, also includes: